

1/28

	1	11 15
ζ	QSFGLLDPK	LCYLLDG--
	369	
CD4: ζ	--PTWSTPVHADPK	LCYLLDG--
	1	
γ	LGEPQ	LCYILDA--
	369	
CD4: γ	--PTWSTPVHADPQ	LCYILDA--

Fig. 1a

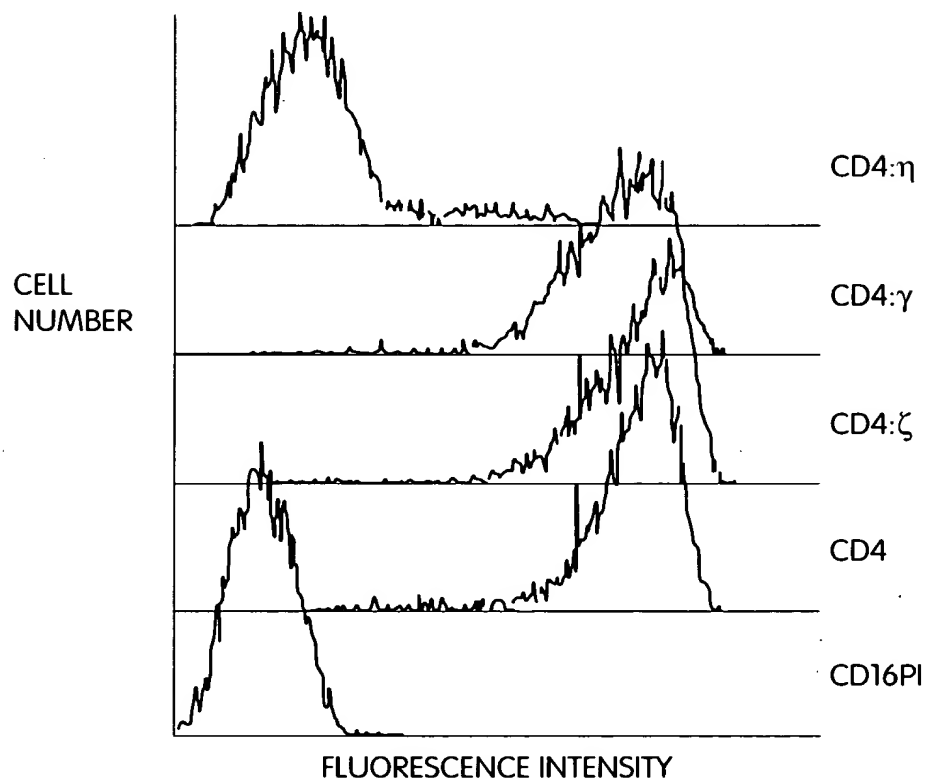


Fig. 1b

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
CRAFTSMAN		

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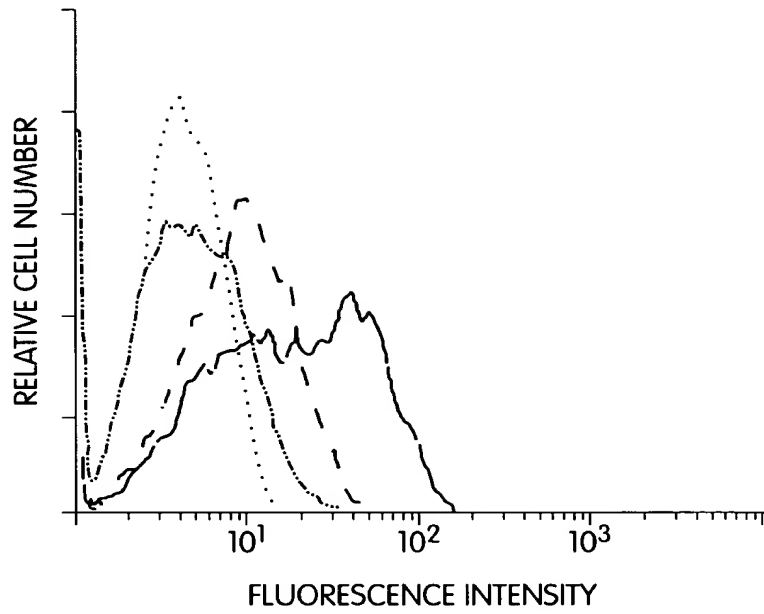


Fig. 2

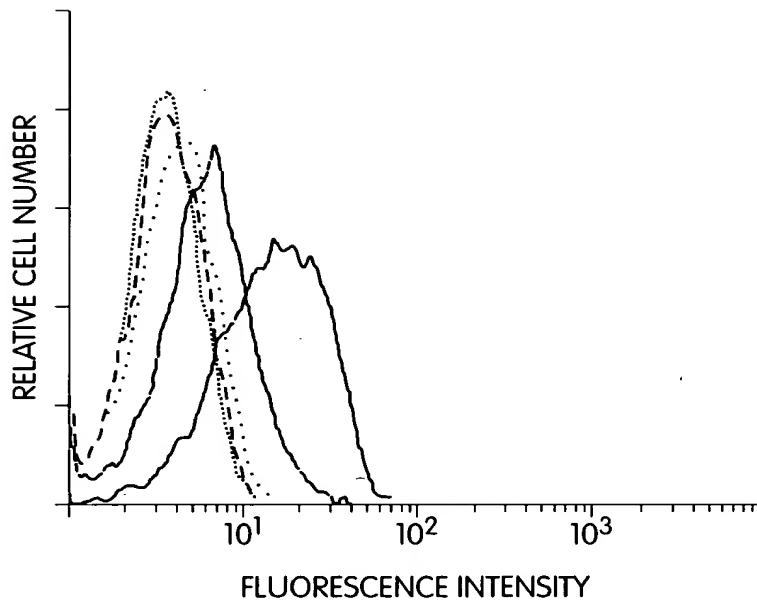


Fig. 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS

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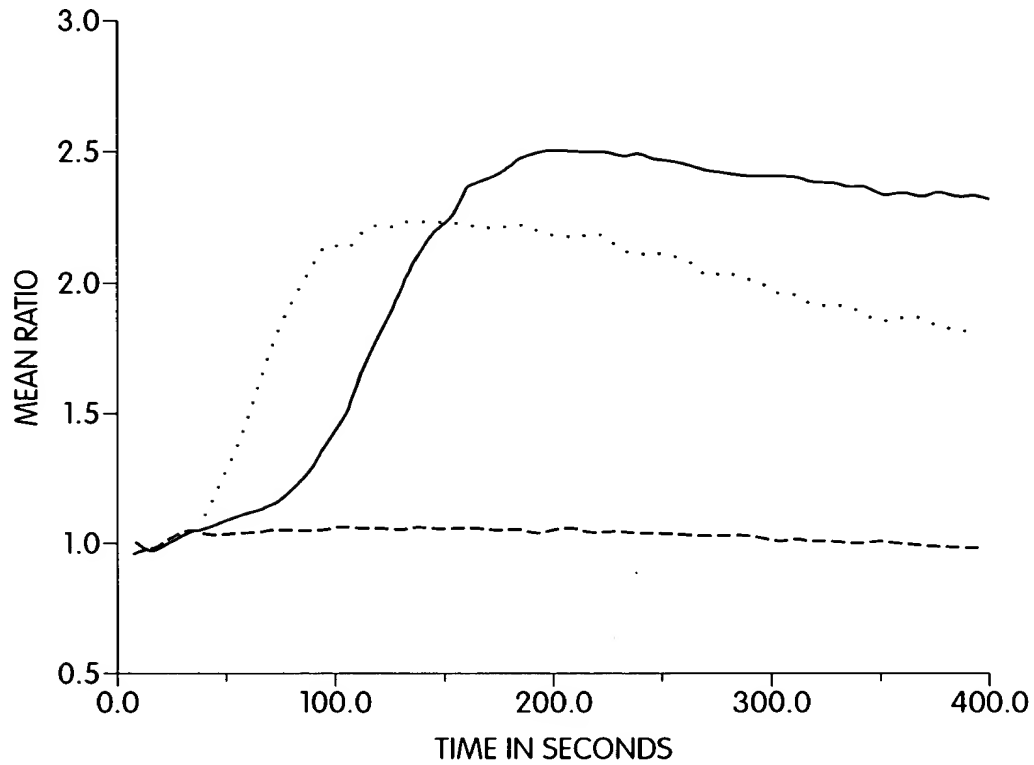


Fig. 4a

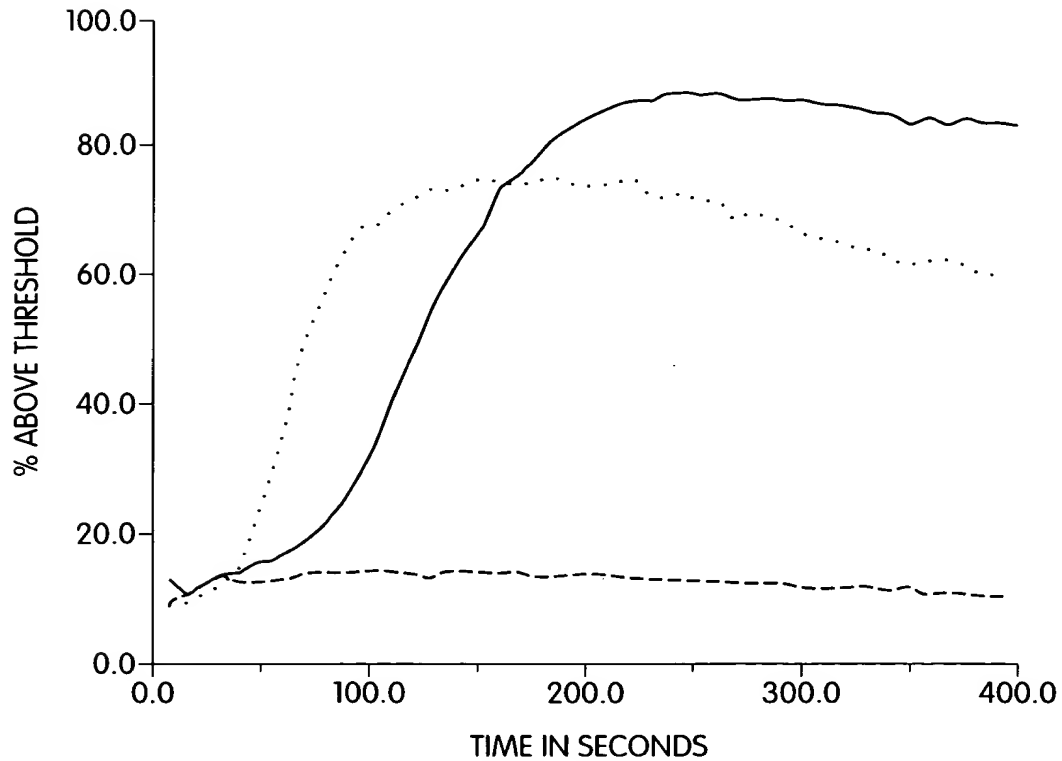


Fig. 4b

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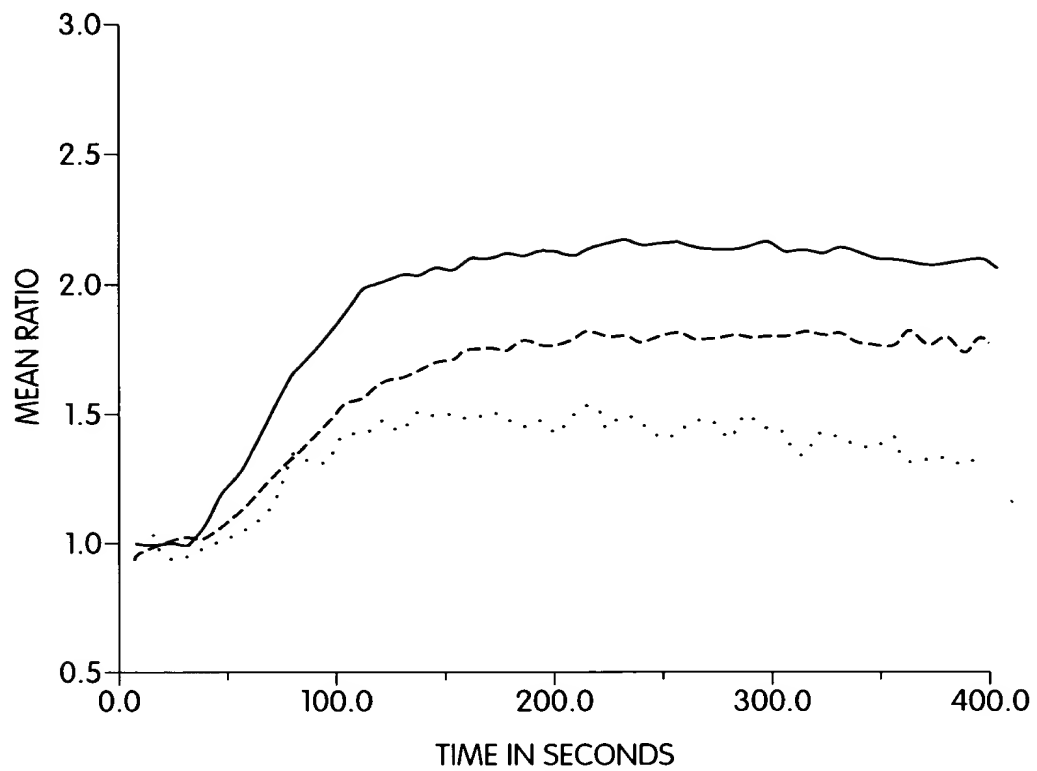


Fig. 4c

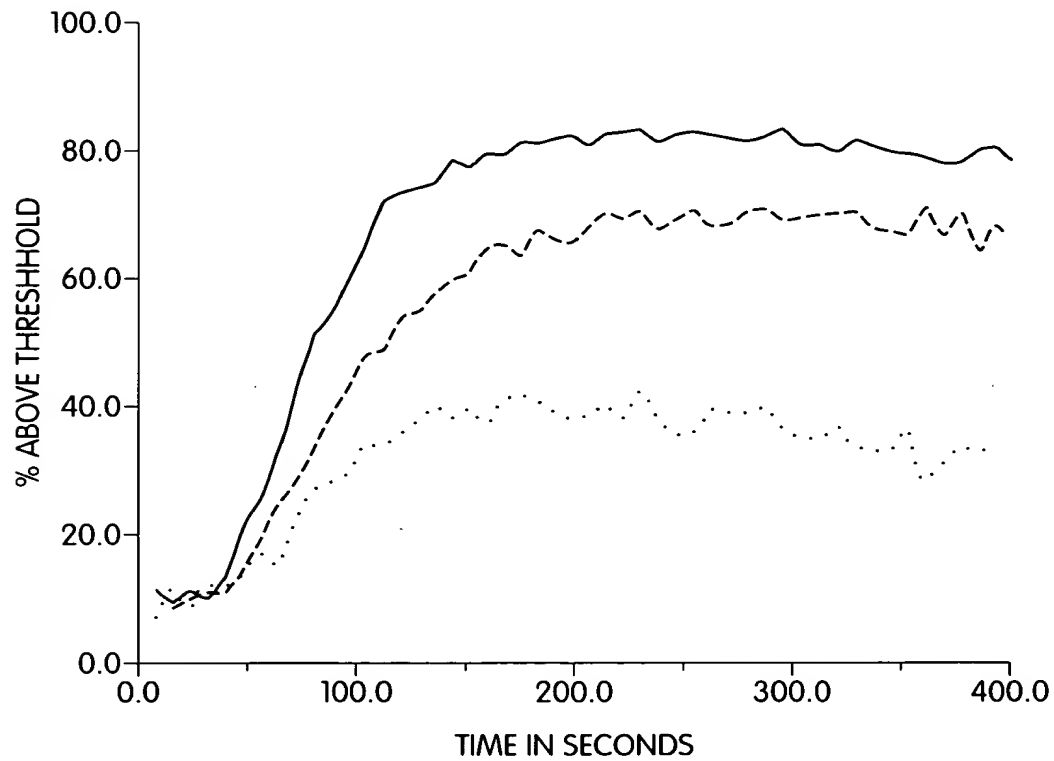


Fig. 4d

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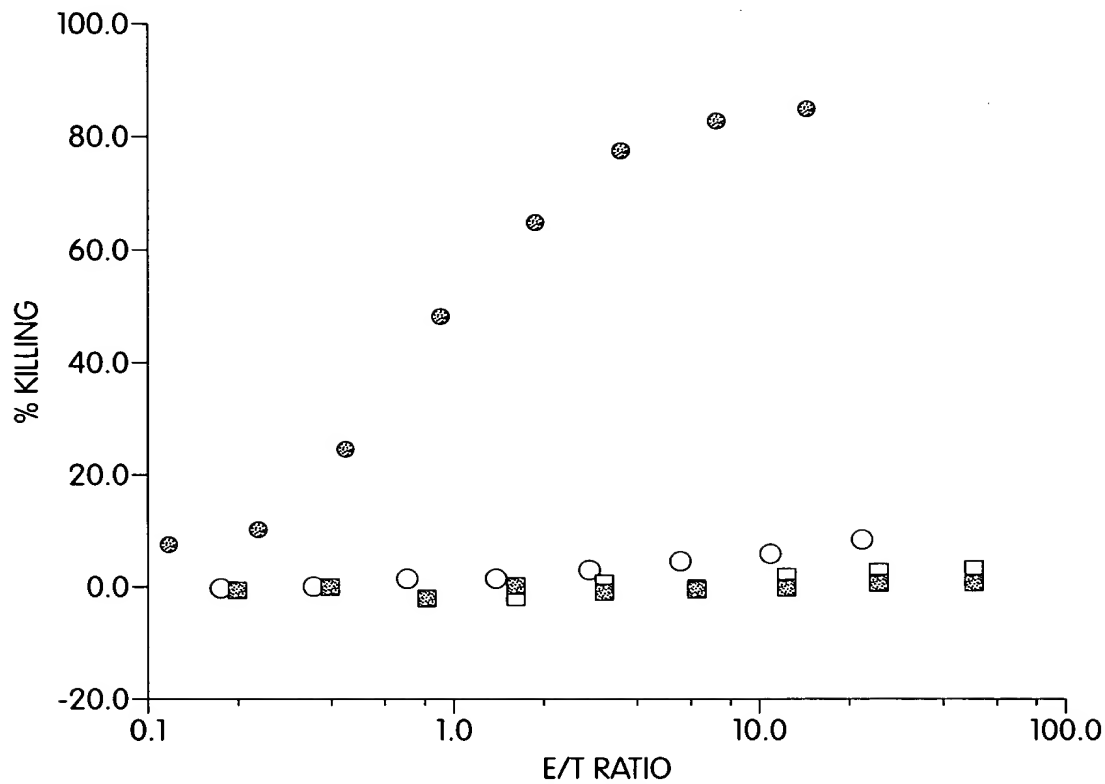


Fig. 5a

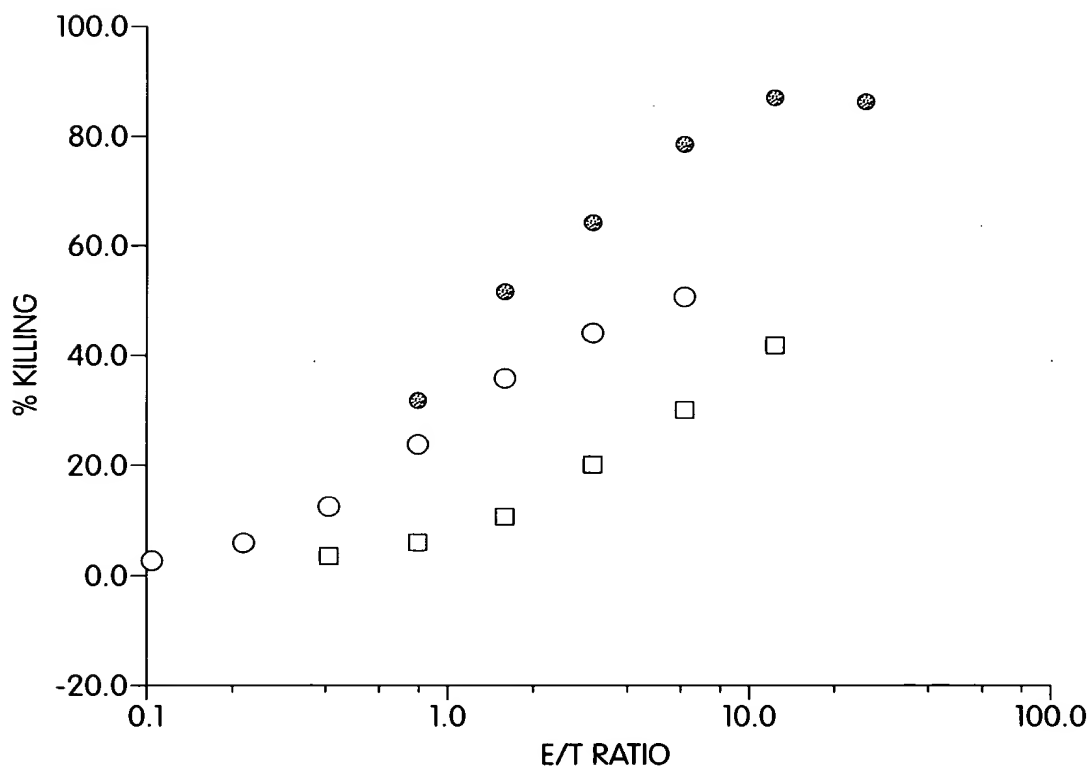


Fig. 5b

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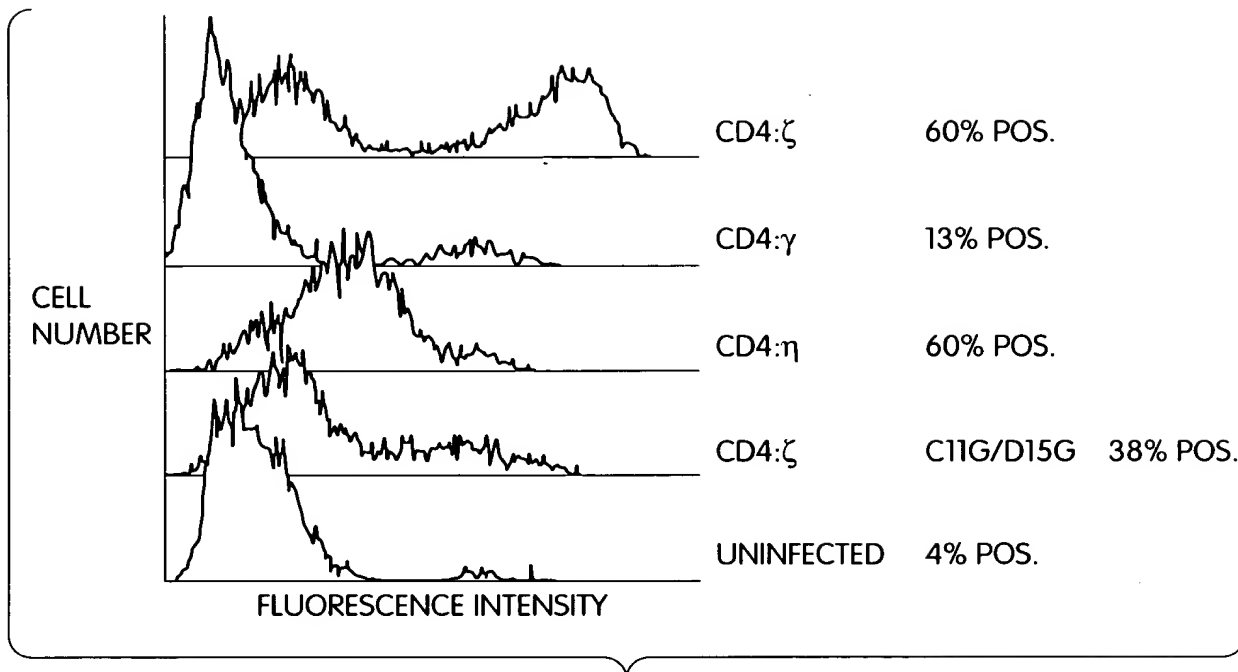


Fig. 5c

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS

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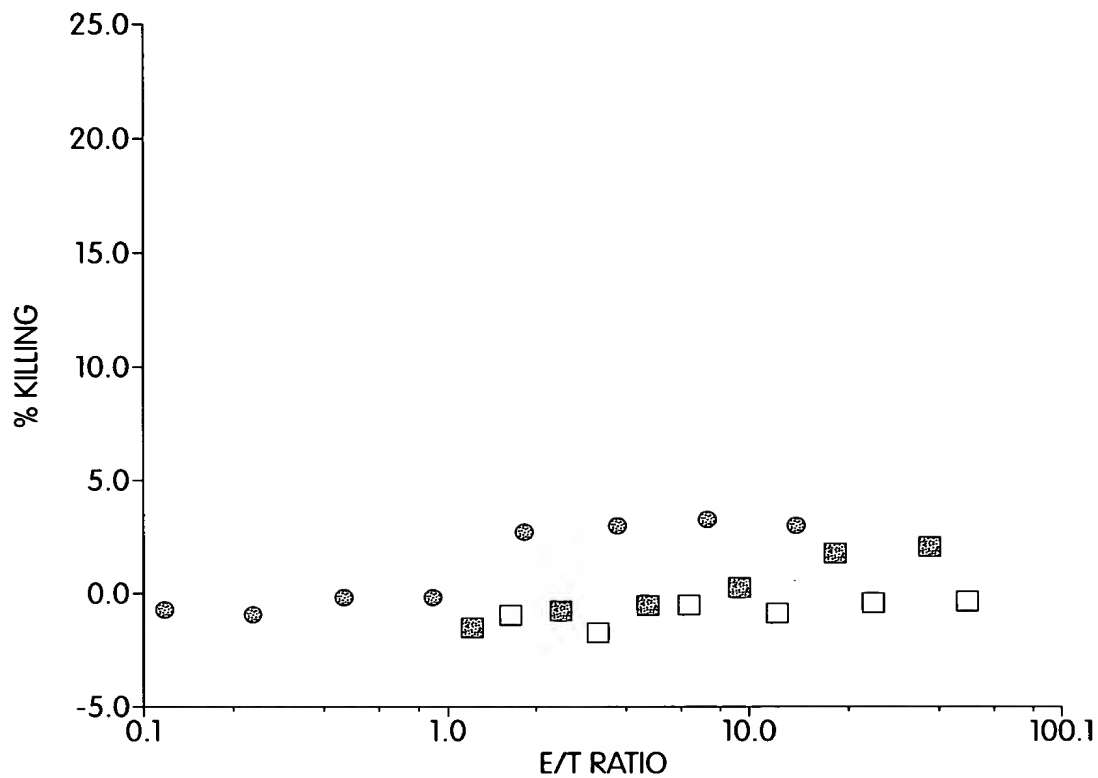


Fig. 6a

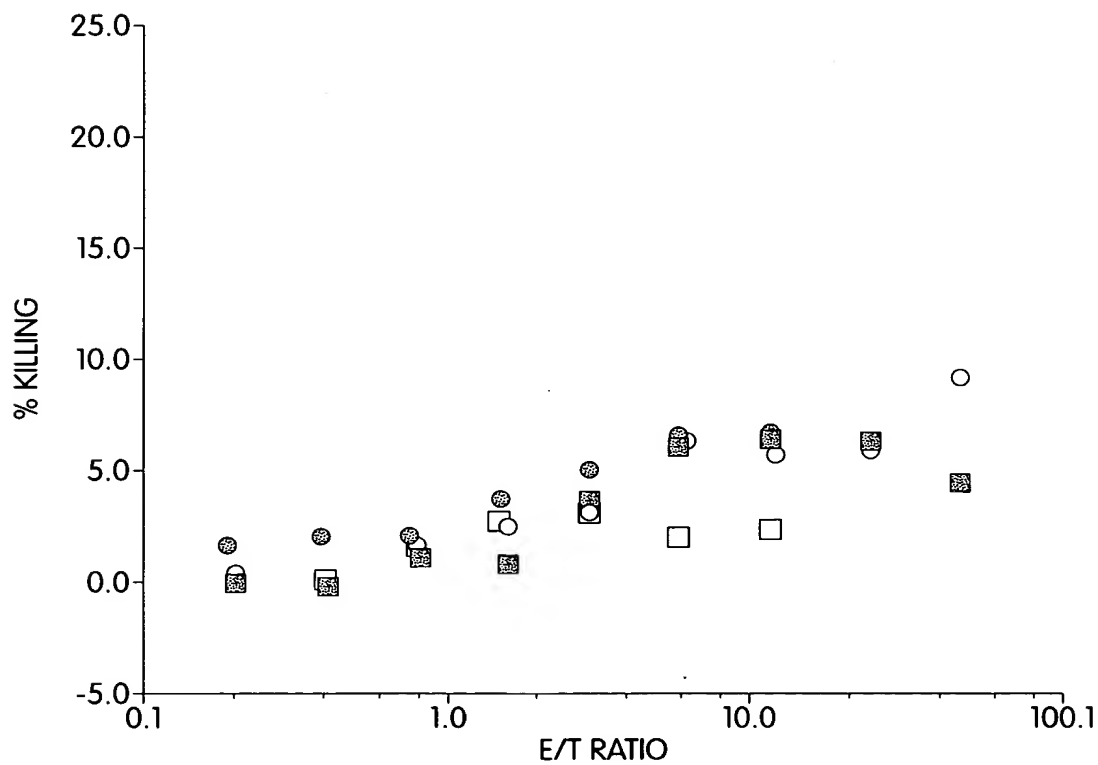


Fig. 6b

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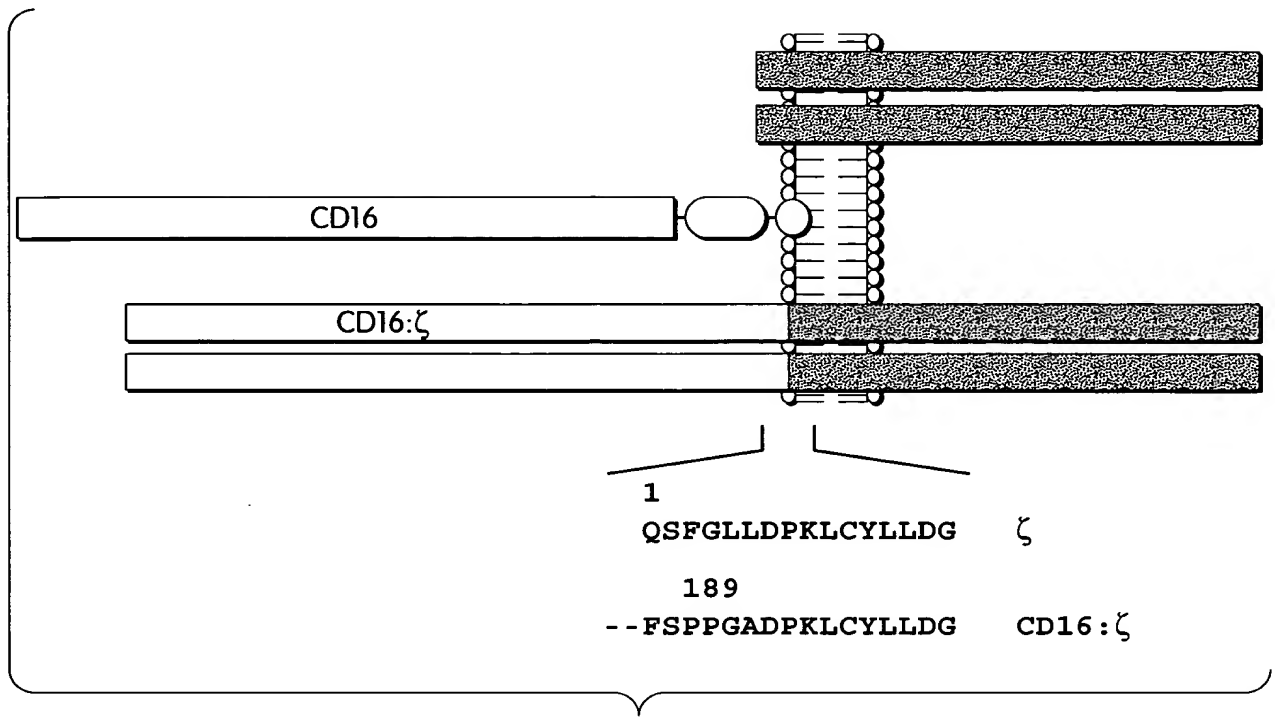


Fig. 7a

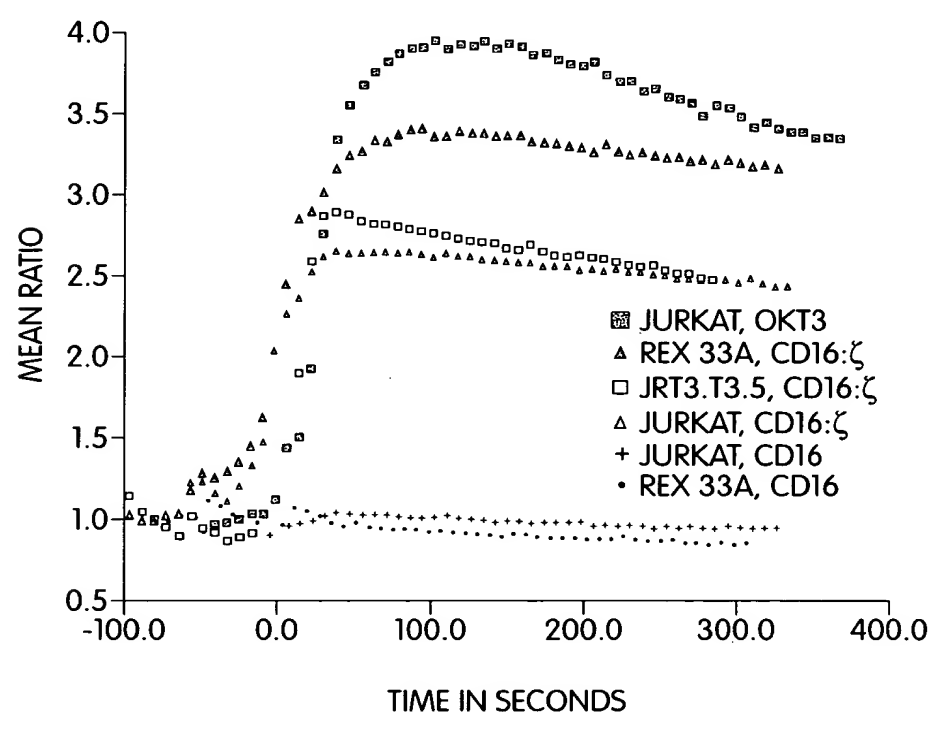


Fig. 7b

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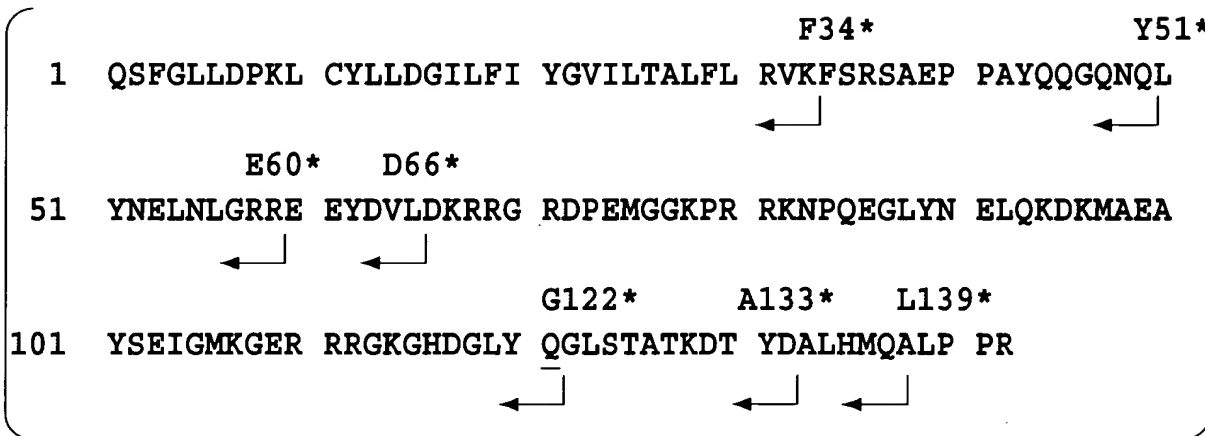


Fig. 8a

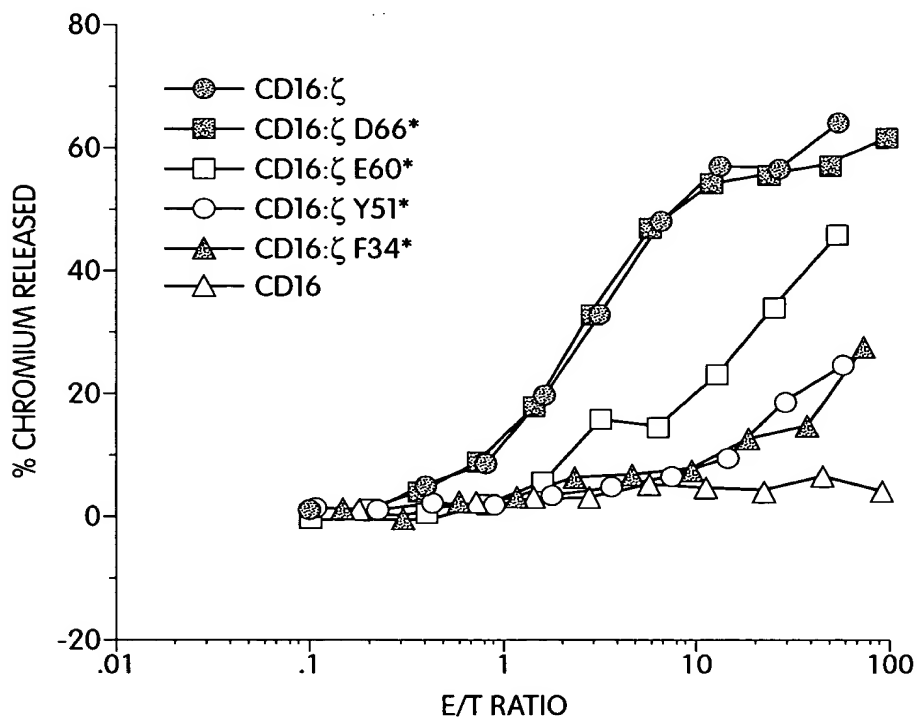


Fig. 8b

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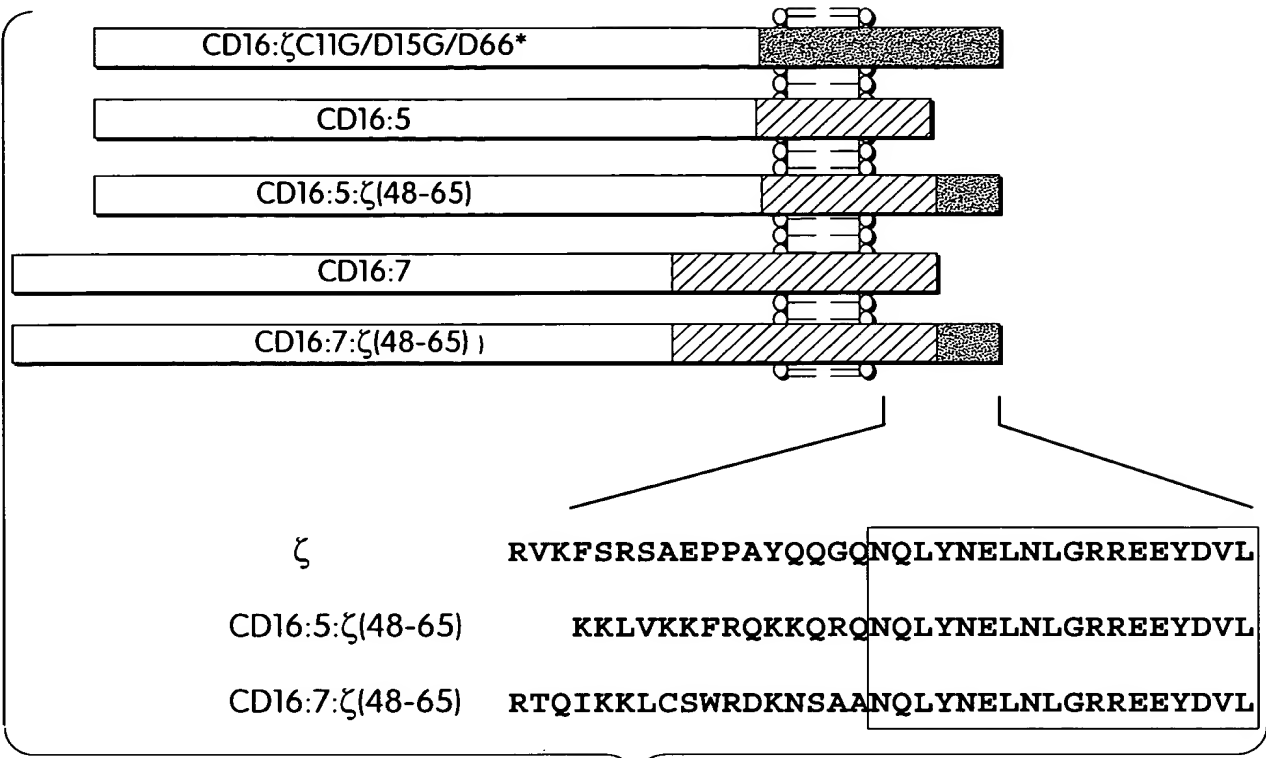


Fig. 9a

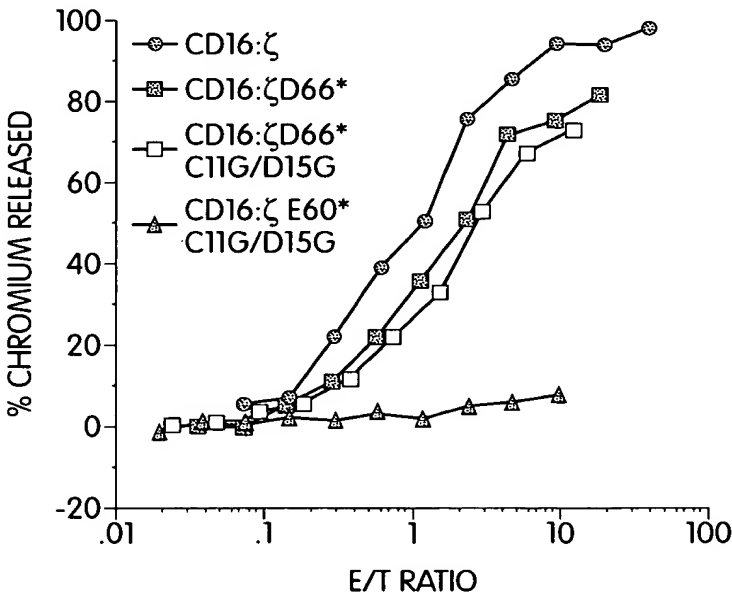


Fig. 9b

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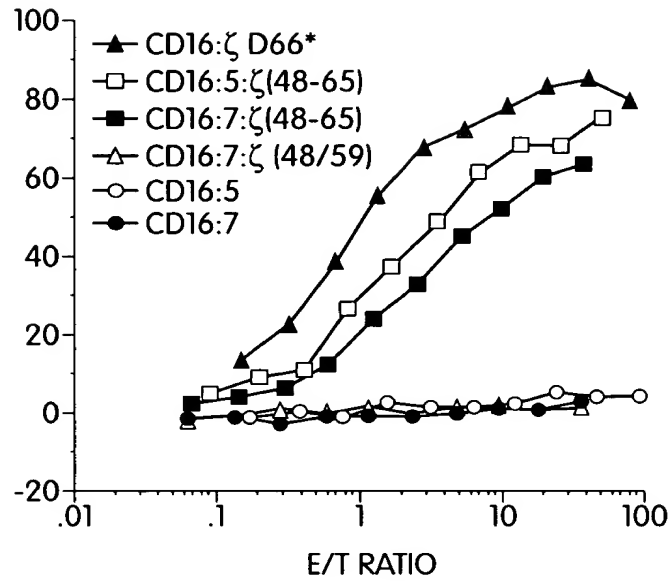


Fig. 9c

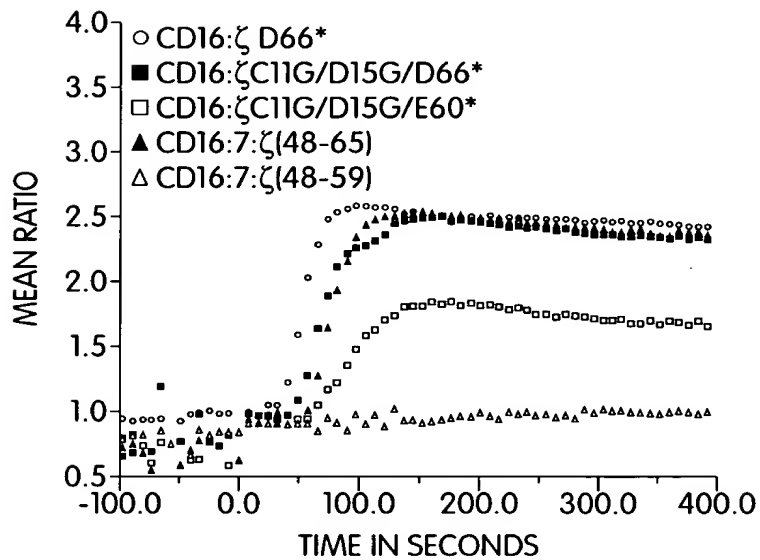


Fig. 9d

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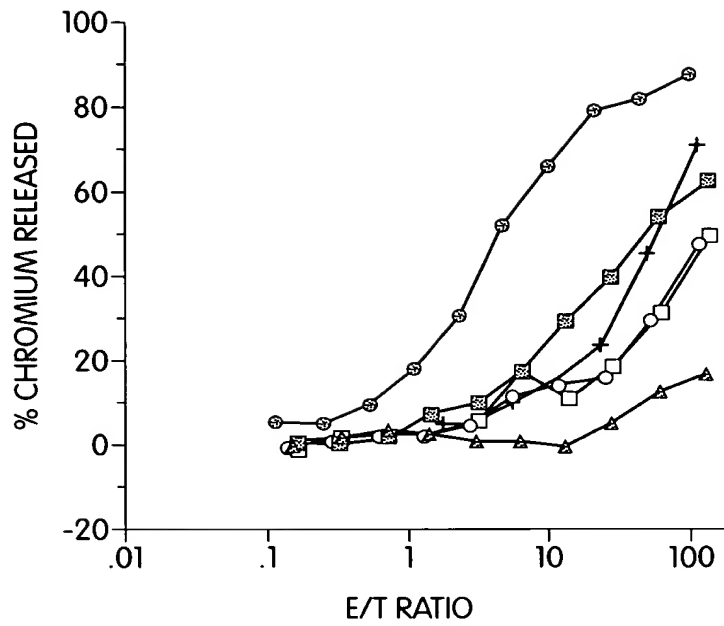


Fig. 10a

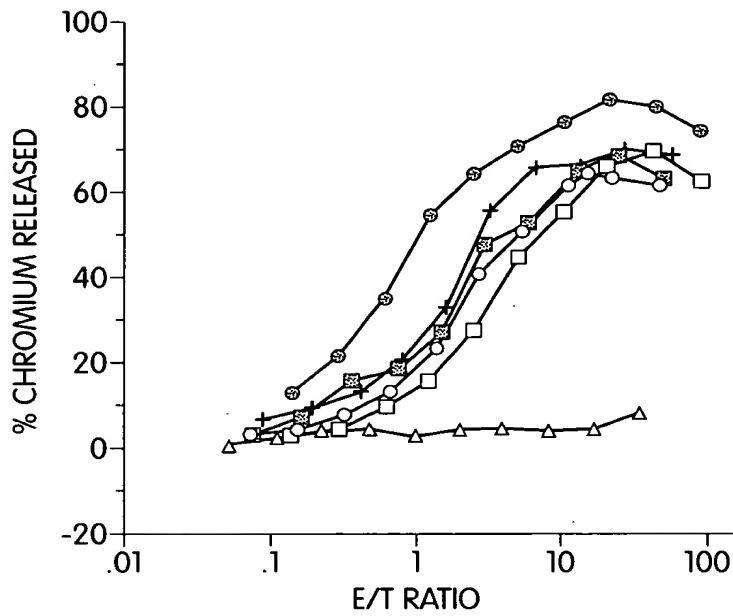


Fig. 10b

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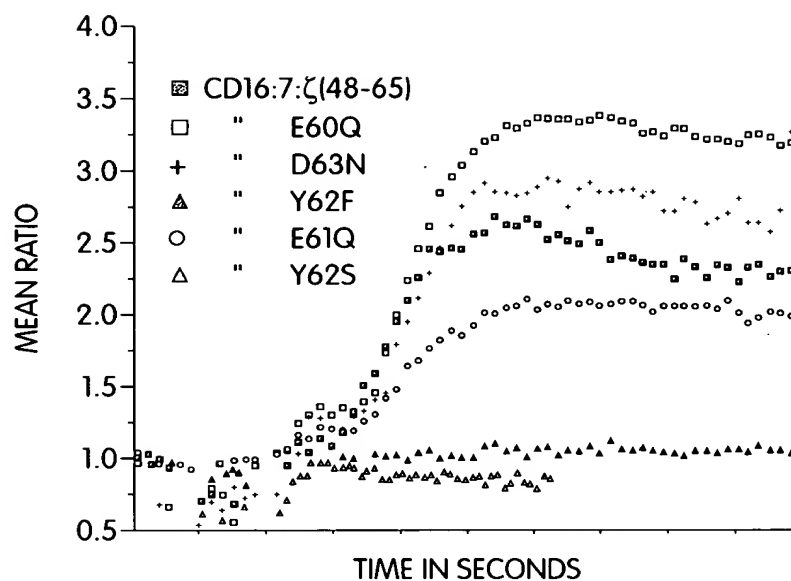


Fig. 10c

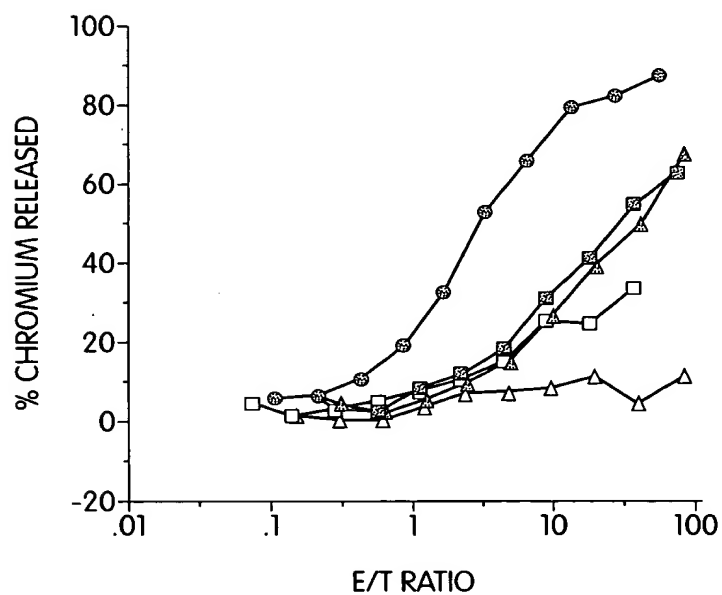


Fig. 10d

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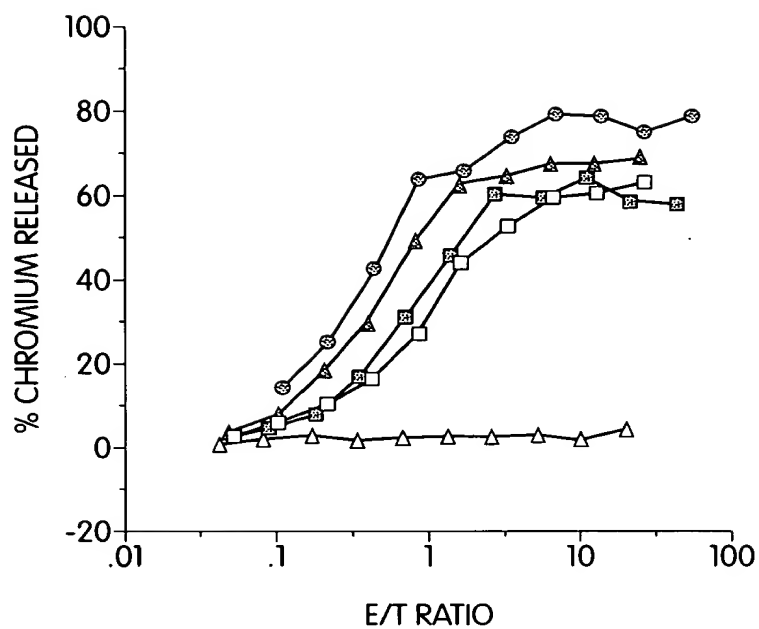


Fig. 10e

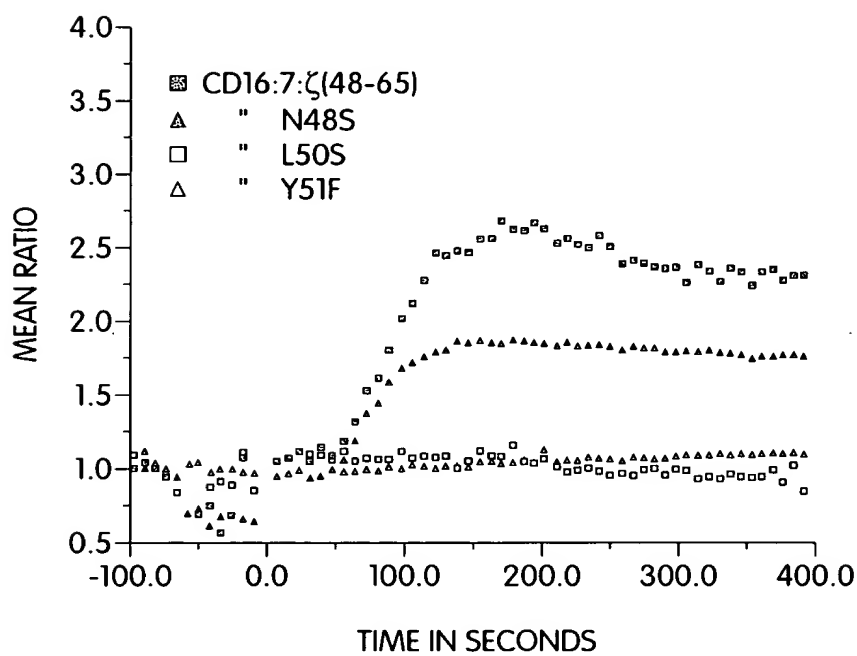


Fig. 10f

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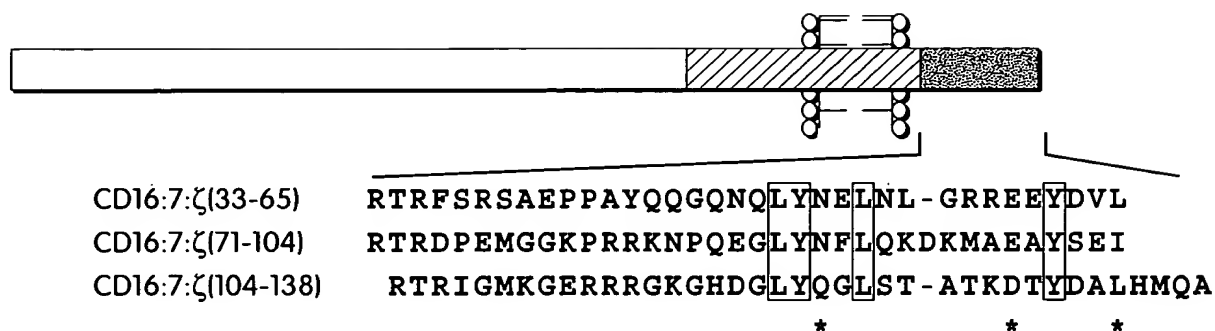


Fig. 11a

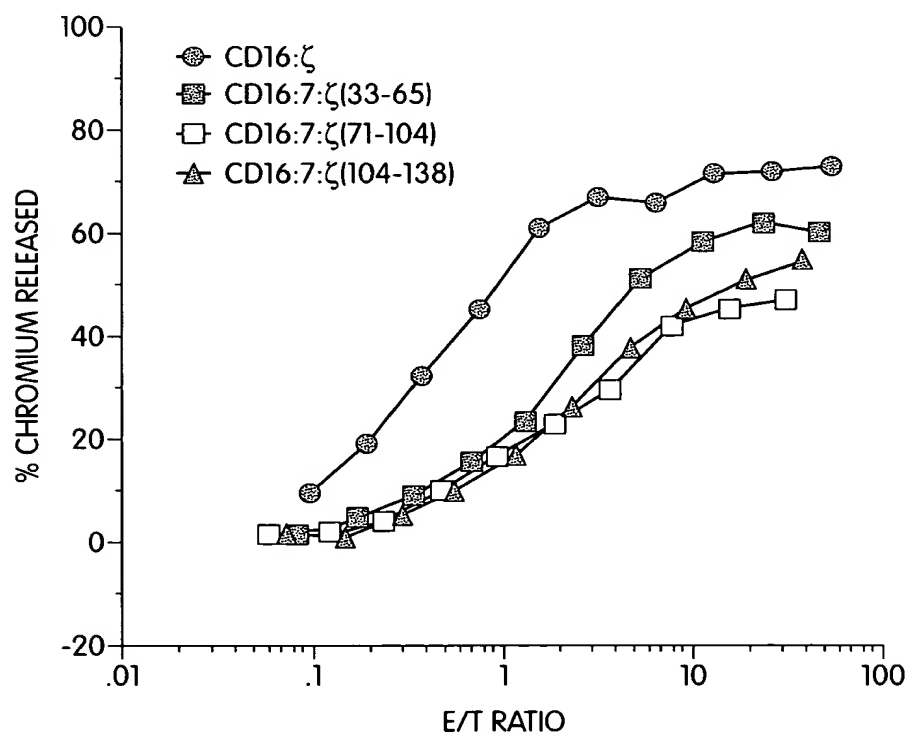


Fig. 11b

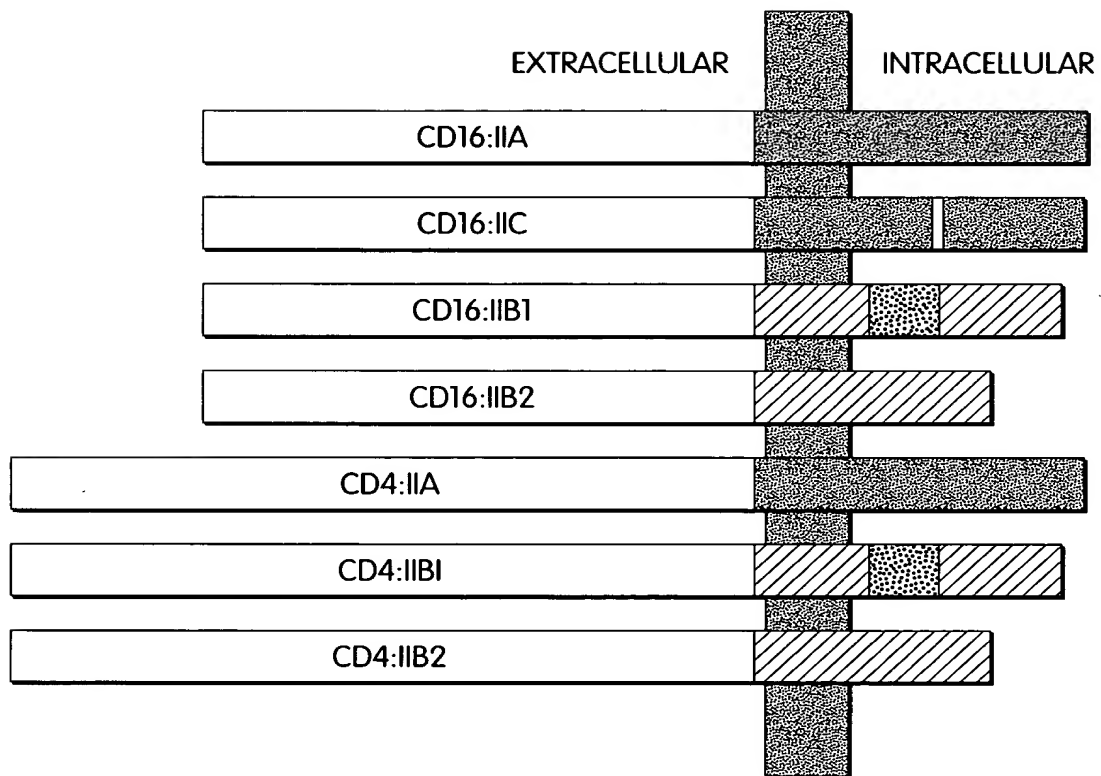


Fig. 12

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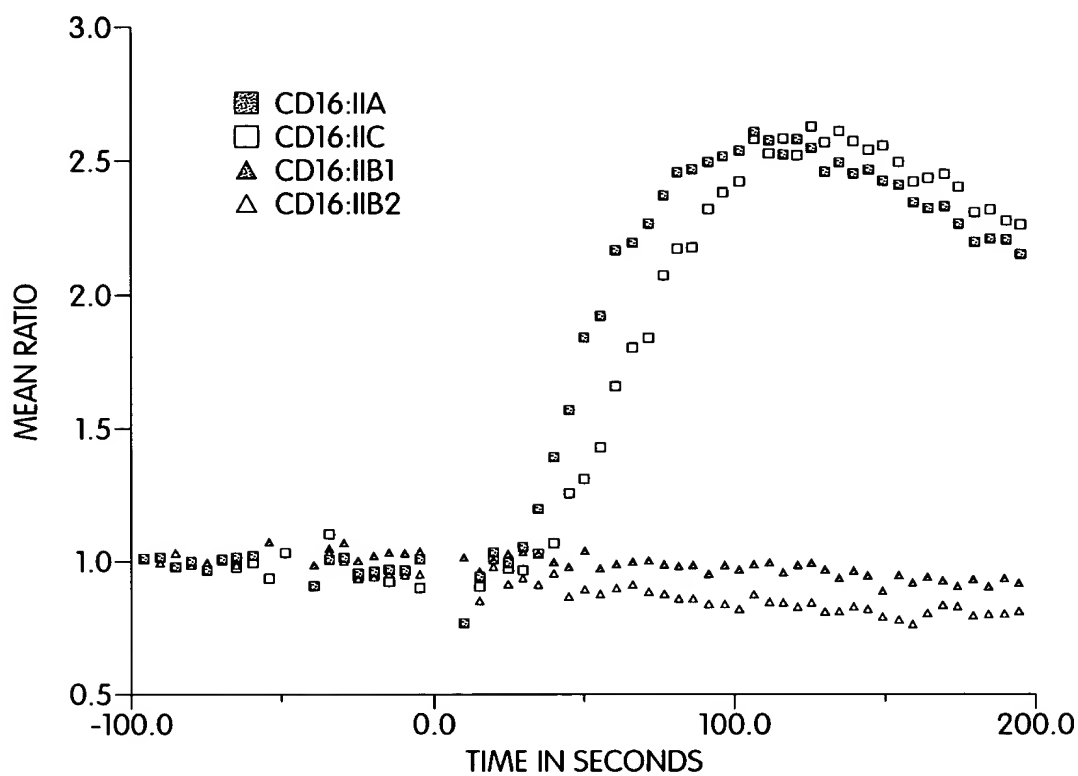


Fig. 13a

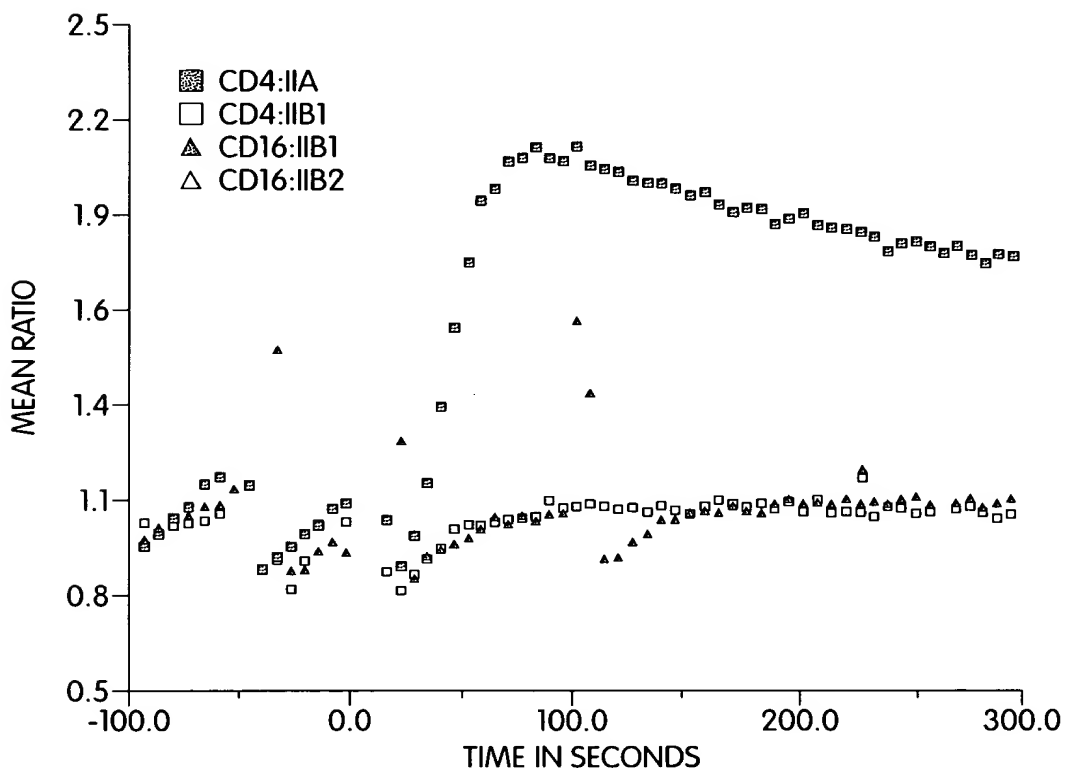


Fig. 13b

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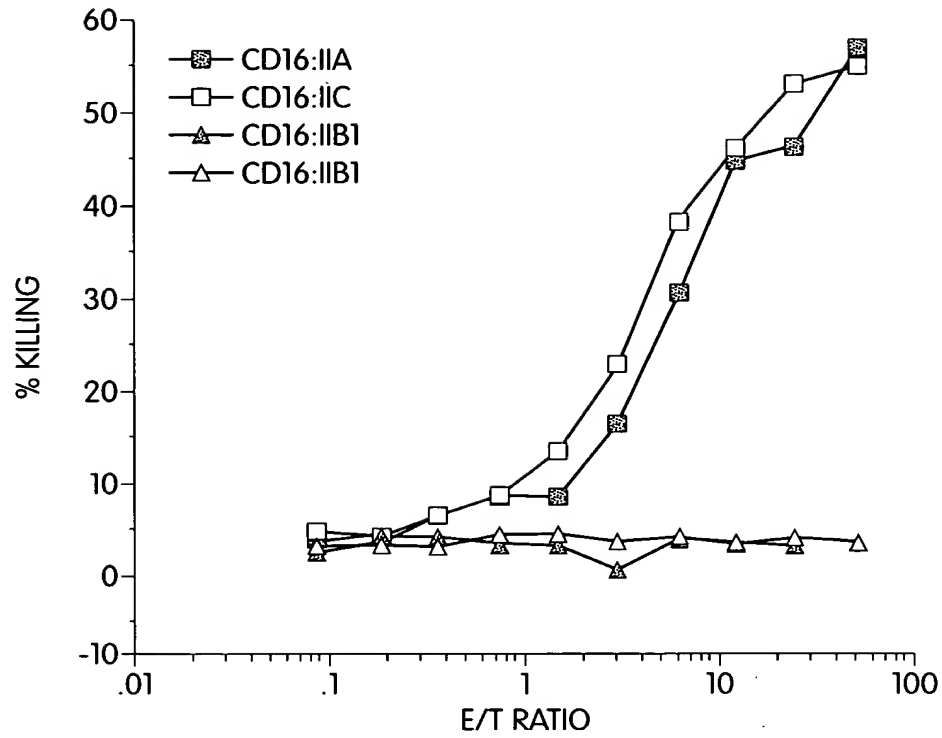


Fig. 14a

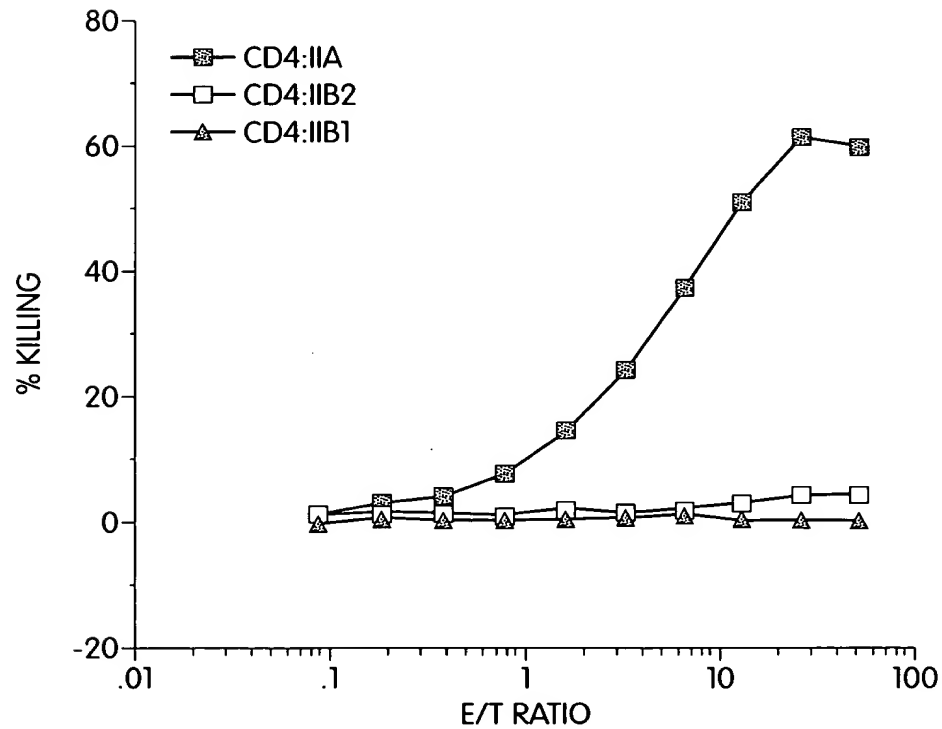


Fig. 14b

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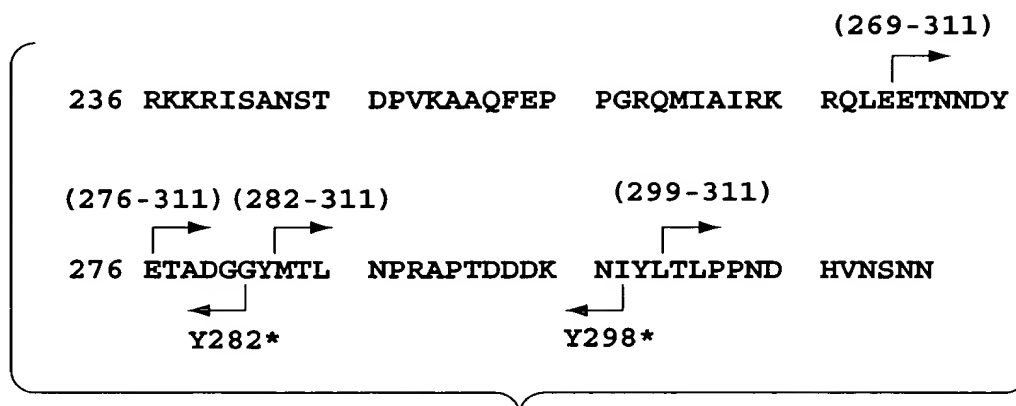


Fig. 15a

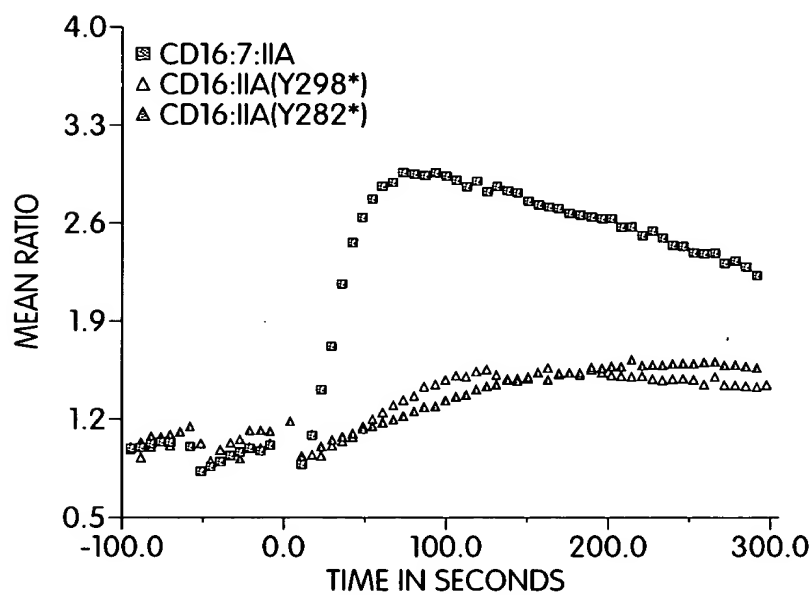


Fig. 15b

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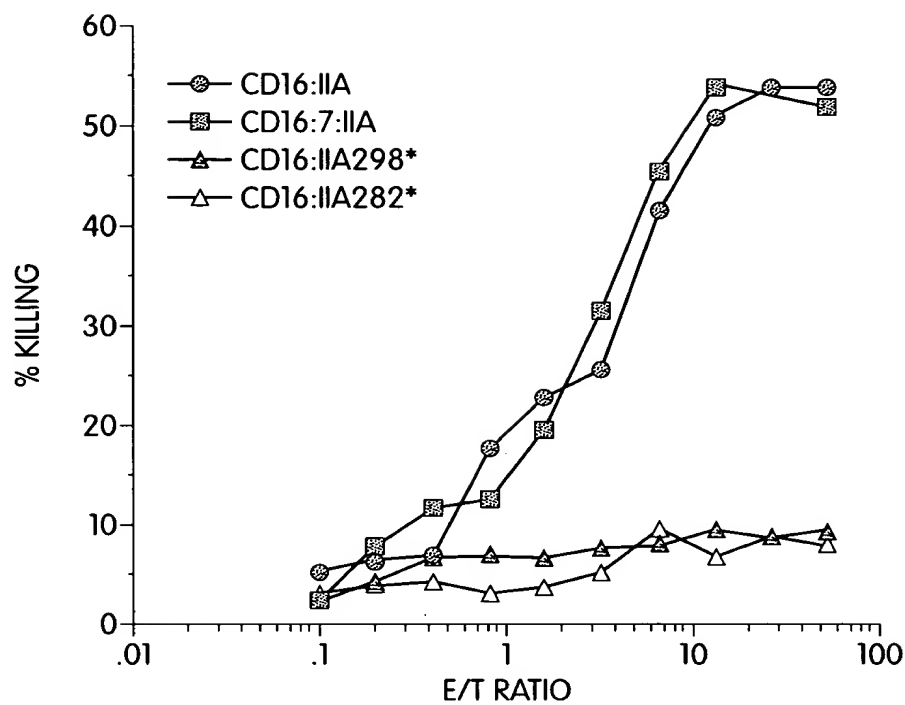


Fig. 15c

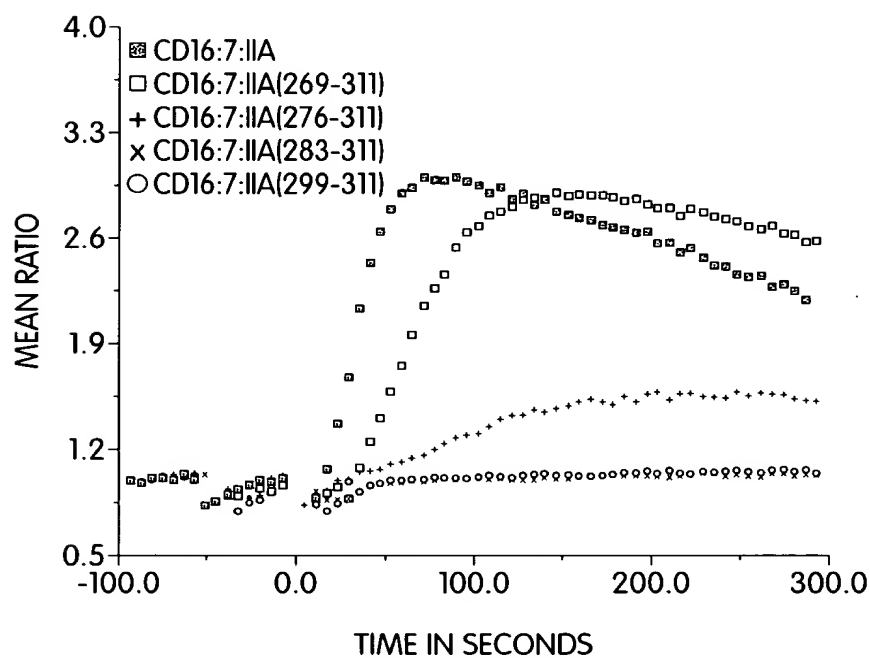


Fig. 15d

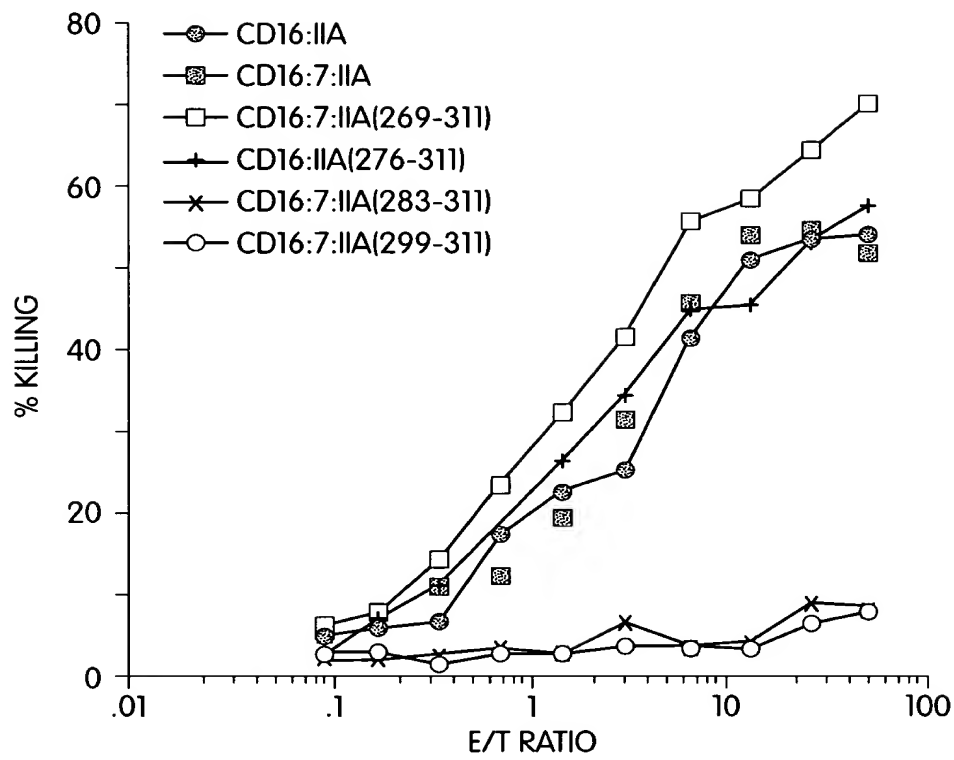


Fig. 15e

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(Seq. ID No: 24)

1	MEHSTFLSGL	VLATLLSQVS	PFKIPIEELE	DRVFN CNTS	ITWVEGTVGT
51	LLSDITRLDL	GKRILDPRI	YRCNGTDIYK	DKESTVQVHY	RMCQSCVEID
101	PATVAGIIVT	DVIATLLLAL	GVFCFAGHET	GRLSGAADTQ	ALLRNDQVYQ
151	PLRDRDDAQY	SHLGGNWARN	K*		

Fig. 16

(Seq ID NO: 25)

1	MEQGKGLAVL	ILAIILLQGT	LAQSIKGNHL	VKVYDYQEDG	SVLLTCDAEA
51	KNITWFKD GK	MIGFLTEDKK	KWNLG SNAKD	PRGMYQCKGS	QNKSKPLQVY
101	YRMCQNCIEL	NAATISGFLF	AEIVSIFVLA	VG VYFIAGQD	GVRQSRASDK
151	QTL LPNDQLY	QPLKDREDDQ	YSHLQGNQLR	RN*	

Fig. 17

(Seq ID No: 26)

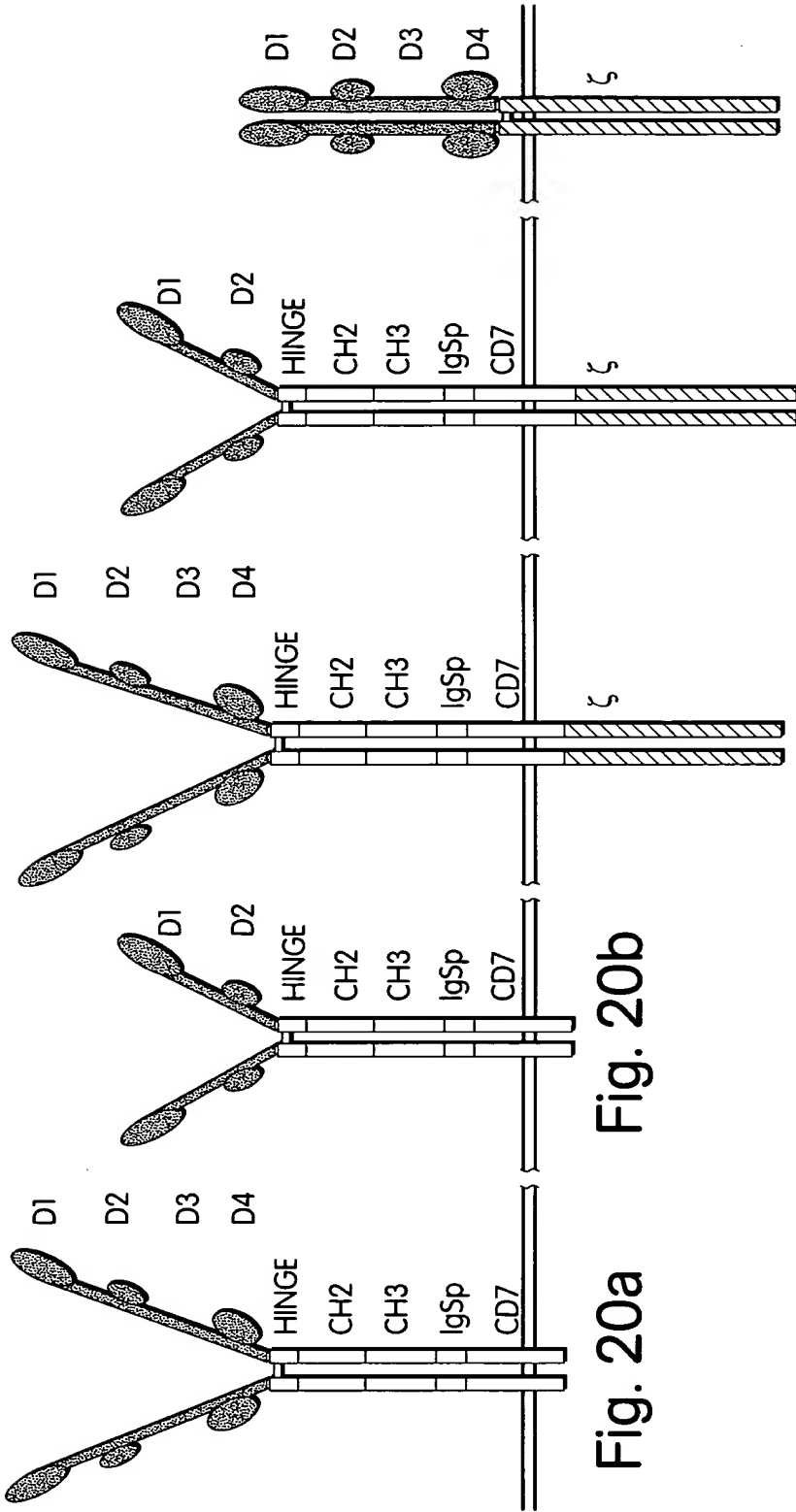
1	MPGGLEALRA	LPLLLFLSYA	CLGPGCQALR	VEGGPPSLTV	NLGEEARLTC
51	ENNGRNPNIT	WWFSLQSNIT	WPPVPLGPGQ	GTTGQLFFPE	VNKNTGACTG
101	CQVIENNILK	RSCGTYLRVR	NPVPRPFLDM	GEGTKNRIIT	AEGIILLFCA
151	VVP GTLLLFR	KRWQNEKFGV	DMPDDYEDEN	LYEGLNLDDC	SMYEDISRGL
201	QGT YQDVGNL	HIGDAQLEKP	*		

Fig. 18

(Seq ID No: 27)

1	MATLVLSMP	CHWLLFLLLL	FSGEPVPAMT	SSDLPLNFQG	SPCSQIWQHP
51	RFAAKKRSSM	VKFHCYTNHS	GALTWFRKRG	SQQPQELVSE	EGRIVQTQNG
101	SVYTLTIQNI	QYEDNGIYFC	KQKCD SANHN	VTDSCGTELL	VLGFSTLDQL
151	KRRNTLKDGI	ILIQTLIIIL	FIIVPIFLLL	DKDDGKAGME	EDHTYEGLNI
201	DQTATYEDIV	TLRTGEVKWS	VGEHPGQE*		

Fig. 19



BamHI/BstYI

Bgl2/BstYI

G GAT CCC AAG GCC AGG CTA AAG CCG AAG CCG CGA AGG CCG AGG CTA AGG CCG AAG CAG ATC TG
D P K A E A K A E A K A E A D L

Fig. 28

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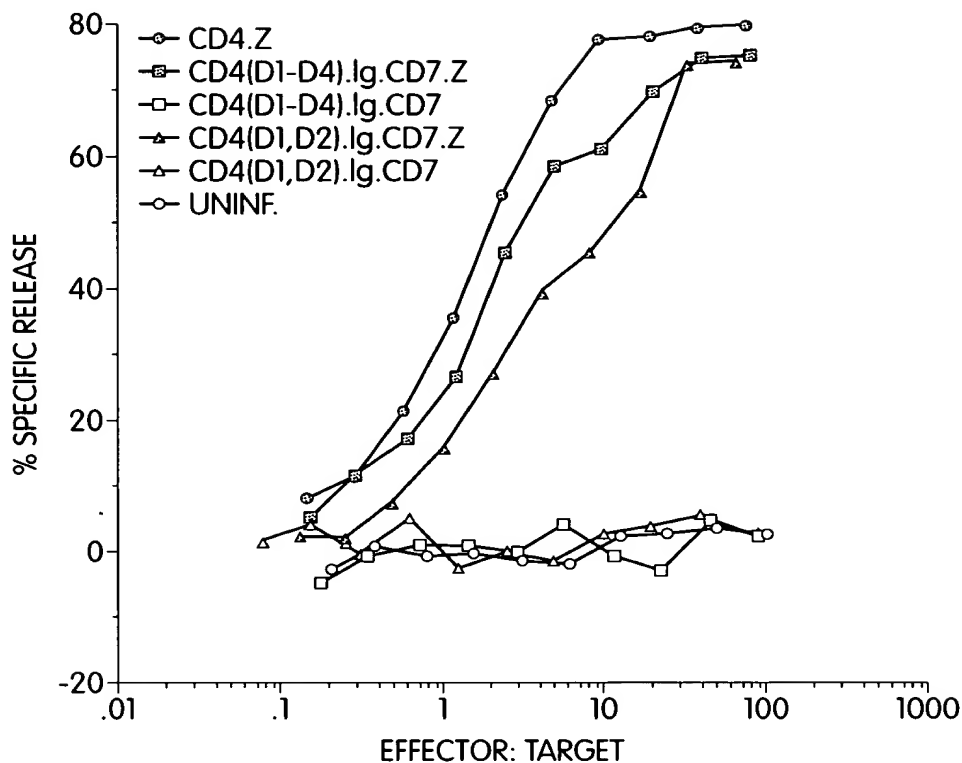


Fig. 21

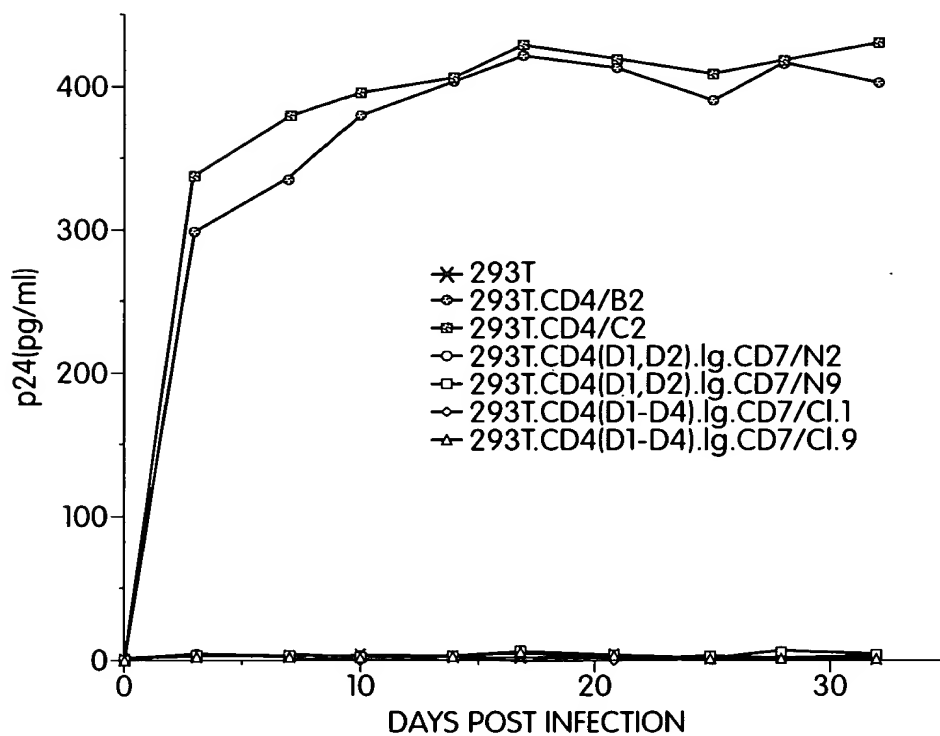


Fig. 22

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D1 - D4 of CD4

Nucleic Acid Sequence

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GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCTG CCTCCCTCGG 101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201
GGCAAAAAG GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA 251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301
ATCAGGGCTC CTTCTTAACT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
AGAAGGAGGA GGTGCAATTG CTAGTGTTTC GATTGACTGC CAACTCTGAC 501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC 551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC 601
AGGGGGGGAA GACCTCTCTC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
AGACATCGTG GTGCTAGCTT TCCAGAAGGC CTCCAGCATA GTCTATAAGA 751
AAGAGGGGGA ACAGGTGGAG TTCTCCTTCC CACTCGCCTT TACAGTTGAA 801
AAGCTGACGG GCAGTGCGGA GCTGTGGTGG CAGGCGGAGA GGGCTTCCTC 851
CTCCAAGTCT TGGATCACCT TTGACCTGAA GAACAAGGAA GTGTCTGTAA 901
AACGGGTTAC CCAGGACCCT AAGCTCCAGA TGGGCAAGAA GCTCCCGCTC 951
CACCTCACCC TGCCCCAGGC CTTGCCTCAG TATGCTGGCT CTGGAAACCT 1001
CACCTGGCC CTTGAAGCGA AAACAGGAAA GTTGTCATCAG GAAGTGAACC 1051
TGGTGGTGAT GAGAGCCACT CAGCTCCAGA AAAATTTGAC CTGTGAGGTG 1101
TGGGGACCCA CCTCCCCTAA GCTGATGCTG AGCTTGAAAC TGGAGAACA 1151
GGAGGCAAAG GTCTCGAAGC GGGAGAAGCC GGTGTGGGTG CTGAACCCTG 1201
AGGCGGGGAT GTGGCAGTGT CTGCTGAGTG ACTCGGGACA GGTCTGCTG 1251
GAATCCAACA TCAAGGTTCT GCCCACATGG TCCACCCCGG TGCACGCGGA 1301
TCCC (SEQ ID NO: 28)
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Amino Acid Sequence

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MNRGVPPFRL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKKSIIQ 51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRD DSRRSLWDQG NFPLIKNLKL 101
IEDSDTYICE VEDQKEEVQL LVFGLTANS DTHLLQGQSLT LTLESPPGSS 151
PSVQCRSPRG KNIQGGKTL S VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV 201
VLAFAQASSI VYKKEGEQVE FSFPLAFTVE KLTGSGELWW QAERASSSKS 251
WITFDLKNKE VSVKRVTD P KLQMGKYLPL HLTLPQALPQ YAGSGNLTLA 301
LEAKTGKHLQ EVNLVVMRAT QLQKNLTCEV WGPTSPKLML SLKLENKEAK 351
VSKREKPVWV LNPEAGMWQC LLSDSGQVLL ESNIKVLPTW STPVHADP
(SEQ ID NO: 29)
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Fig. 23

D1 - D2 of CD4

Nucleic Acid Sequence

GCCTGTTTGA GAAGCAGCGG GCAAGAAAGA CGCAAGCCCA GAGGCCCTGC 51
CATTTCTGTG GGCTCAGGTC CCTACTGGCT CAGGCCCTG CCTCCCTCGG 101
CAAGGCCACA ATGAACCGGG GAGTCCCTTT TAGGCACTTG CTTCTGGTGC 151
TGCAACTGGC GCTCCTCCCA GCAGCCACTC AGGGAAACAA AGTGGTGCTG 201
GGCAAAAAG GGGATACAGT GGAAGTACC TGTACAGCTT CCCAGAAGAA 251
GAGCATACAA TTCCACTGGA AAAACTCCAA CCAGATAAAG ATTCTGGGAA 301
ATCAGGGCTC CTTCTTAAGT AAAGGTCCAT CCAAGCTGAA TGATCGCGCT 351
GACTCAAGAA GAAGCCTTTG GGACCAAGGA AACTTCCCCC TGATCATCAA 401
GAATCTTAAG ATAGAAGACT CAGATACTTA CATCTGTGAA GTGGAGGACC 451
AGAAGGAGGA GGTGCAATTG CTAGTGTTTCG GATTGACTGC CAACTCTGAC 501
ACCCACCTGC TTCAGGGGCA GAGCCTGACC CTGACCTTGG AGAGCCCCCC 551
TGGTAGTAGC CCCTCAGTGC AATGTAGGAG TCCAAGGGGT AAAAACATAC 601
AGGGGGGGAA GACCCTCTCC GTGTCTCAGC TGGAGCTCCA GGATAGTGGC 651
ACCTGGACAT GCACTGTCTT GCAGAACCAG AAGAAGGTGG AGTTCAAAAT 701
AGACATCGTG GTGCTAGCT (SEQ ID NO: 30)

Amino Acid Sequence

MNRGVPFRHL LLVLQLALLP AATQGNKVVL GKKGDTVELT CTASQKRSIQ 51
FHWKNSNQIK ILGNQGSFLT KGPSKLNDRD DSRRSLWDQG NFPLIIKNLK 101
IEDSDTYICE VEDQKEEVQL LVFGLTANS DTHLLQGQSLT LTLESPPGSS 151
PSVQCRSPRG KNIQGGKTLS VSQLELQDSG TWTCTVLQNQ KKVEFKIDIV 201
VLA (SEQ ID NO: 31)

Fig. 24

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Hinge, CH2, and CH3 Domains of Human IgG1

Nucleic Acid Sequence

```
GCTAGCAGAG CCCAAATCTT GTGACAAAAC TCACACATGC CCACCGTGCC 51
CAGCACCTGA ACTCCTGGGG GGACCGTCAG TCTTCCTCTT CCCCCCAAAA 101
CCCAAGGACA CCCTCATGAT CTCCCGGACC CCTGAGGTCA CATGCGTGGT 151
GGTGGACGTG AGCCACGAAG ACCCTGAGGT CAAGTTCAAC TGGTACGTGG 201
ACGGCGTGGA GGTGCATAAT GCCAAGACAA AGCCGCGGGA GGAGCAGTAC 251
AACAGCACGT ACCGGGTGGT CAGCGTCCTC ACCGTCCTGC ACCAGGACTG 301
GCTGAATGGC AAGGAGTACA AGTGCAAGGT CTCCAACAAA GCCCTCCCAG 351
CCCCCATCGA GAAAACCATC TCCAAAGCCA AAGGGCAGCC CCGAGAACCA 401
CAGGTGTACA CCCTGCCCCC ATCCCGGGAT GAGCTGACCA AGAACCAGGT 451
CAGCCTGACC TGCCTGGTCA AAGGCTTCTA TCCAGCGAC ATCGCCGTGG 501
AGTGGGAGAG CAATGGGCAG CCGGAGAACA ACTACAAGAC CACGCCTCCC 551
GTGCTGGACT CCGACGGCTC CTTCTTCCTC TACAGCAAGC TCACCGTGGA 601
CAAGAGCAGG TGGCAGCAGG GGAACGTCTT CTCATGCTCC GTGATGCATG 651
AGGCTCTGCA CAACCACTAC ACGCAGAAGA GCCTCTCCCT GTCTCCGGGG 701
CTGCAACTGG ACGAGACCTG TGCTGAGGCC CAGGACGGGG AGCTGGACGG 751
GCTCTGGACG ACGGATCC (SEQ ID NO: 32)
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Amino Acid Sequence

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EPKSCDKTHT CPPCPAPELL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD 51
VSHEDPEVKF NWYVDGVEVH NAKTKPREEQ YNSTYRVVSV LTVLHQDWLN 101
GKEYKCKVSN KALPAPIEKT ISKAKGQPRE PQVYTLPPSR DELTKNQVSL 151
TCLVKGFYPS DIAVEWESNG QPENNYKTP PVLDSGGSFF LYSKLTVDKS 201
RWQQGNVFSC SVMHEALHNNH YTQKSLSLSP GLQLDETCAE AQDGELDGLW 251
TTDP (SEQ ID NO: 33)
```

Fig. 25

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CD7 Transmembrane Domain

Nucleic Acid Sequence

CCAAGGGCCT CTGCCCTCCC TGCCCCACCG ACAGGCTCCG CCCTCCCTGA 51
 CCCGCAGACA GCCTCTGCCC TCCCTGACCC GCCAGCAGCC TCTGCCCTCC 101
 CTGCGGCCCT GGCGGTGATC TCCTTCCTCC TCGGGCTGGG CCTGGGGGTG 151
 GCGTGTGTGC TGGCGAGGAC GCGT (SEQ ID NO: 34)

Amino Acid Sequence

PRASALPAPP TGSALPDPQT ASALPDPPAA SALPAALAVI SFLGLGLGV 51
 ACVLARTR (SEQ ID NO: 35)

Fig. 26

Zeta Intracellular Domain

Nucleic Acid Sequence

ACGCGTTTCA GCAGGAGCGC AGAGCCCCC GCGTACCAGC AGGGCCAGAA 51
 CCAGCTCTAT AACGAGCTCA ATCTAGGACG AAGAGAGGAG TACGATGTTT 101
 TGGACAAGAG ACGTGGCCGG GACCCTGAGA TGGGGGGAAA GCCGAGAAGG 151
 AAGAACCCTC AGGAAGGCCT GTACAATGAA CTGCAGAAAG ATAAGATGGC 201
 GGAGGCCTAC AGTGAGATTG GGATGAAAGG CGAGCGCCGG AGGGGCAAGG 251
 GGCACGATGG CCTTTACCAG GGTCTCAGTA CAGCCACCAA GGACACCTAC 301
 GACGCCCTTC ACATGCAGGC CCTGCCCCCT CGCTAAAGCG GCCGC
 (SEQ ID NO: 36)

Amino Acid Sequence

TRFSRSAEPP AYQQGQNQLY NELNLGRREE YDVLDKRRGR DPEMGGKPRR 51
 KNPQEGLYNE LQDKMAEAY SEIGMYGERR RGKGHGGLYO GLSTATKDTY 101
 DALHMQALPP R (SEQ ID NO: 37)

Fig. 27